The X-ray Crystal Structure of FinO, a Repressor of Bacterial Conjugation

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Introduction: The conjugative transfer of F-like plasmids in *E. coli* is regulated by the two-component FinO/P system. FinP is an antisense RNA that represses the translation of TraJ, a transcription factor that is required for conjugation. FinO binds to both FinP and *traJ* mRNA, stabilising FinP against endonucleolytic degradation and facilitating FinP – *traJ* RNA interactions.

Methods and Materials: We used multiwavelength anomalous dispersion techniques to determine the X-ray crystal structure of Se-methionyl FinO.

Results and **Conclusions**: FinO adopts a largely helical, extended conformation (**Figure 1**). Previous work demonstrated that both the N- and C-terminal helices contact RNA. Our crystal structure shows that these two helices interact and present a contiguous RNA contact surface. Based on this structure, we predicted that the N-terminus of the first helix could interact with and stabilize a sense-antisense RNA interactions. This prediction is supported by the behavior of FinO mutants in an in vitro RNA association assay.

References: A. Ghetu, M. Gubbins, L. Frost, J. Glover, "The X-ray Crystal Structure of FinO, a Repressor of Bacterial Conjugation." Nat. Struct. Biol. 7, 565, 2000.

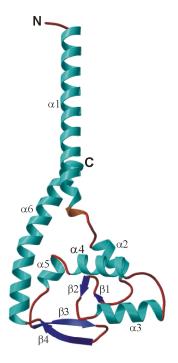


Figure 1. A ribbons diagram of FinO(26-186).